

<!--StartFragment-->

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 9, 2006, 03:58:59 ; Search time 222.529 Seconds
 (without alignments)
 106.841 Million cell updates/sec

Title: US-09-819-144A-2
 Perfect score: 268
 Sequence: 1 MAAGPRPGAPCRAGAPTIVL.....SSPARATLGKPLVLNDYSLN 52

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	268	100.0	52	2	AAY39293 CSA-1 cho
2	77	28.7	209	7	ABM87430 Rice abio
3	74	27.6	16	2	AAY39295 Polypepti
4	73.5	27.4	337	7	ADC32784 Human nov
5	73.5	27.4	675	9	AEA52600 Human Rab
6	73.5	27.4	791	5	ABP65089 Hypoxia-r
7	73.5	27.4	791	8	ADN03640 Antipsori
8	73.5	27.4	791	8	ADP22972 PRO polyp
9	73.5	27.4	863	6	ABP98856 Human str
10	73.5	27.4	863	7	ADC31071 Human nov
11	73.5	27.4	863	7	ADE48296 Human MIC
12	73.5	27.4	863	7	ADE48308 Human MIC
13	73.5	27.4	863	8	ABM82355 Tumour-as
14	72.5	27.1	173	7	ABO76575 Pseudomon
15	71.5	26.7	76	3	AAG28488 Zea mays

16	71	26.5	19938	6	ABP76682	Abp76682	Streptomy
17	69.5	25.9	210	4	AAU48625	Aau48625	Propionib
18	69.5	25.9	210	6	ABM45144	Abm45144	Propionib
19	68	25.4	315	5	ABU05772	Abu05772	M. tuberc
20	68	25.4	315	8	ABM79606	Abm79606	M tubercu
21	67.5	25.2	135	4	AAO01165	Aao01165	Human pol
22	67.5	25.2	137	7	ABO81794	Abo81794	Pseudomon
23	67	25.0	1321	9	ADV97797	Adv97797	Murine pr
24	66	24.6	228	7	ABO79635	Abo79635	Pseudomon
25	65.5	24.4	923	7	ADD18710	Add18710	Human dis
26	65.5	24.4	923	8	ADO19848	Ado19848	Human PRO
27	65.5	24.4	924	8	ADU06294	Adu06294	Novel bro
28	65	24.3	166	7	ABO68030	Abo68030	Pseudomon
29	65	24.3	205	7	ABO82421	Abo82421	Pseudomon
30	65	24.3	345	7	ABO77022	Abo77022	Pseudomon
31	64.5	24.1	146	7	ABO77184	Abo77184	Pseudomon
32	64.5	24.1	149	7	ABO82120	Abo82120	Pseudomon
33	64.5	24.1	309	4	ABG12975	Abg12975	Novel hum
34	64.5	24.1	341	8	ADK71091	Adk71091	Human MP2
35	64	23.9	137	3	AAG28496	Aag28496	Zea mays
36	63.5	23.7	223	8	ADY06811	Ady06811	Plant ful
37	63.5	23.7	377	9	ADY85271	Ady85271	Human ort
38	63.5	23.7	478	7	AAO30817	Aao30817	Human cel
39	63.5	23.7	721	7	ABO79547	Abo79547	Pseudomon
40	63	23.5	53	5	ABP01580	Abp01580	Human ORF
41	63	23.5	128	7	ADB64958	Adb64958	Human pro
42	63	23.5	128	7	ADM03909	Adm03909	Human pro
43	63	23.5	128	9	AEC86839	Aec86839	Human cDN
44	63	23.5	613	7	ABO71209	Abo71209	Pseudomon
45	63	23.5	1129	7	ABO73584	Abo73584	Pseudomon

<!--EndFragment-->

<!--StartFragment-->

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OM protein - protein search, using sw model

Run on: December 9, 2006, 03:58:59 ; Search time 68.4706 Seconds
 (without alignments)
 106.841 Million cell updates/sec

Title: US-09-819-144A-8
 Perfect score: 83
 Sequence: 1 RRQTLSHGSSSPARAC 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	83	100.0	16	2	AAY39295 Polypepti
2	74	89.2	52	2	AAY39293 CSA-1 cho
3	47	56.6	275	3	AAY74422 Neisseria
4	47	56.6	276	3	AAY74421 Neisseria
5	47	56.6	276	3	AAY74420 Neisseria
6	45	54.2	407	6	ABU08934 Human tum
7	45	54.2	407	7	ADM05759 Human pro
8	45	54.2	407	8	ADI79418 Human MAG
9	45	54.2	407	9	AEC88689 Human cDN
10	44	53.0	145	6	AAE37292 Human gen
11	43	51.8	199	7	ABO71484 Pseudomon
12	43	51.8	220	3	AAG32041 Arabidops
13	43	51.8	236	3	AAG32040 Arabidops
14	43	51.8	284	3	AAG32039 Arabidops
15	43	51.8	427	7	ABO73903 Pseudomon

16	43	51.8	854	7	AAE38184	Aae38184	Fruit fly
17	42	50.6	64	4	AAU58002	Aau58002	Propionib
18	42	50.6	64	6	ABM54521	Abm54521	Propionib
19	42	50.6	85	4	AAU21041	Aau21041	Human nov
20	42	50.6	147	7	ABO77336	Abo77336	Pseudomon
21	42	50.6	152	4	AAU40386	Aau40386	Propionib
22	42	50.6	152	6	ABM36905	Abm36905	Propionib
23	42	50.6	215	7	ABO75620	Abo75620	Pseudomon
24	42	50.6	566	8	ADX78475	Adx78475	Plant ful
25	42	50.6	843	7	ABO70181	Abo70181	Pseudomon
26	41.5	50.0	314	5	AAU99417	Aau99417	Human ECS
27	41.5	50.0	345	7	ABO68244	Abo68244	Pseudomon
28	41	49.4	57	4	AAU64156	Aau64156	Propionib
29	41	49.4	57	6	ABM60675	Abm60675	Propionib
30	41	49.4	70	4	AAU51187	Aau51187	Propionib
31	41	49.4	70	6	ABM47706	Abm47706	Propionib
32	41	49.4	112	4	AAU66094	Aau66094	Propionib
33	41	49.4	112	6	ABM62613	Abm62613	Propionib
34	41	49.4	155	5	ABP55326	Abp55326	Human qui
35	41	49.4	178	5	ABP41446	Abp41446	Human ova
36	41	49.4	213	7	ABO73901	Abo73901	Pseudomon
37	41	49.4	349	7	ABO81915	Abo81915	Pseudomon
38	41	49.4	412	8	ADT60756	Adt60756	Plant pol
39	41	49.4	470	5	AAE19560	Aae19560	Equine he
40	41	49.4	740	4	AAB94340	Aab94340	Human pro
41	41	49.4	740	7	ADJ70657	Adj70657	Human hea
42	41	49.4	813	3	AAG52554	Aag52554	Arabidops
43	41	49.4	831	7	ABO76155	Abo76155	Pseudomon
44	41	49.4	835	4	AAB35401	Aab35401	Human PG-
45	41	49.4	835	5	ABP69678	Abp69678	Human pol

<!--EndFragment-->

<!--StartFragment-->

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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:02:32 ; Search time 296.706 Seconds
 (without alignments)
 162.116 Million cell updates/sec

Title: US-09-819-144A-2
 Perfect score: 268
 Sequence: 1 MAAGPRPGAPCRAGAPTIVL.....SSPARATLGKPLVLNDYSLN 52

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	77	28.7	190	2	Q2QXN1_ORYSA	Q2qxn1	oryza sativ
2	74	27.6	432	2	Q3VBL7_9SPHN	Q3vbl7	sphingopyxi
3	73.5	27.4	290	2	Q68D58_HUMAN	Q68d58	homo sapien
4	73.5	27.4	350	2	Q641Q8_HUMAN	Q641q8	homo sapien
5	73.5	27.4	367	2	Q3WCT2_9ACTO	Q3wct2	frankia sp.
6	73.5	27.4	863	1	MILK1_HUMAN	Q8n3f8	homo sapien
7	72	26.9	636	2	Q6AYD5_RAT	Q6ayd5	rattus norv
8	71.5	26.7	1581	2	Q4SA50_TETNG	Q4sa50	tetraodon n
9	70	26.1	238	2	Q37PB1_SPHAR	Q37pb1	novosphingo
10	70	26.1	1004	2	Q4P5V3_USTMA	Q4p5v3	ustilago ma
11	69	25.7	1176	2	Q3AZB7_SYNS9	Q3azb7	synechococc
12	68	25.4	315	2	O53831_MYCTU	O53831	mycobacteri
13	68	25.4	315	2	Q7U173_MYCBO	Q7u173	mycobacteri
14	68	25.4	457	2	Q3FJL6_9BURK	Q3fjl6	burkholderi
15	67.5	25.2	311	2	Q3YJ61_SPHPU	Q3yj61	sphenodon p
16	67.5	25.2	391	2	Q98A00_RHILO	Q98a00	rhizobium l
17	67	25.0	316	2	Q378R2_RHOPA	Q378r2	rhodopseudo
18	67	25.0	453	2	Q3W0F4_9ACTO	Q3w0f4	frankia sp.
19	67	25.0	524	2	Q3PPF1_NITHA	Q3ppf1	nitrobacter
20	67	25.0	563	2	Q4UVP4_XANC8	Q4uvp4	xanthomonas
21	67	25.0	563	2	Q8P8E3_XANCP	Q8p8e3	xanthomonas
22	67	25.0	786	2	Q3U214_MOUSE	Q3u214	mus musculu
23	66.5	24.8	1787	2	Q9M4X9_CHLRE	Q9m4x9	chlamydomon

24	66	24.6	272	2	Q743X3_MYCPA	Q743x3 mycobacteri
25	65.5	24.4	1234	2	Q46UQ6_RALEJ	Q46uq6 ralstonia e
26	64.5	24.1	215	2	Q8IV50_HUMAN	Q8iv50 homo sapien
27	64.5	24.1	596	2	Q82NB1_STRAW	Q82nb1 streptomyce
28	64.5	24.1	610	2	Q40Y43_KINRA	Q40y43 kineococcus
29	64.5	24.1	846	2	Q47MT2_THEFY	Q47mt2 thermobifid
30	64	23.9	613	2	Q4WQ64_ASPFU	Q4wq64 aspergillus
31	64	23.9	731	2	Q4Q5C4_LEIMA	Q4q5c4 leishmania
32	63.5	23.7	289	2	Q3WFZ7_9ACTO	Q3wfz7 frankia sp.
33	63.5	23.7	301	2	Q47JT8_DECAR	Q47jt8 dechloromon
34	63.5	23.7	355	2	Q5R9T2_PONPY	Q5r9t2 pongo pygma
35	63.5	23.7	377	2	Q8N3K4_HUMAN	Q8n3k4 homo sapien
36	63.5	23.7	424	2	Q36XS2_RHOPA	Q36xs2 rhodopseudo
37	63.5	23.7	562	2	Q8BQZ7_MOUSE	Q8bqz7 mus musculu
38	63.5	23.7	566	2	Q4B0Z8_9BURK	Q4b0z8 polaromonas
39	63.5	23.7	874	2	Q6PDL7_MOUSE	Q6pdl7 mus musculu
40	63	23.5	128	2	Q8N0Y6_HUMAN	Q8n0y6 homo sapien
41	63	23.5	171	2	Q6K3G1_ORYSA	Q6k3g1 oryza sativ
42	63	23.5	360	1	YBOX2_MOUSE	Q9z2c8 mus musculu
43	63	23.5	373	2	Q7WNE3_BORBR	Q7wne3 bordetella
44	63	23.5	2063	2	Q4QG78_LEIMA	Q4qg78 leishmania
45	62.5	23.3	150	2	Q84ZQ6_ORYSA	Q84zq6 oryza sativ

<!--EndFragment-->

<!--StartFragment-->

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:02:32 ; Search time 91.2941 Seconds
 (without alignments)
 162.116 Million cell updates/sec

Title: US-09-819-144A-8
 Perfect score: 83
 Sequence: 1 RRQTLSHGSSSPARAC 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

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 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	60.2	562	2	Q4Q9F1_LEIMA	Q4q9f1 leishmania
2	50	60.2	682	2	Q4S297_TETNG	Q4s297 tetraodon n
3	48	57.8	391	2	Q9RHC5_BRAJA	Q9rhc5 bradyrhizob
4	47	56.6	409	2	Q984F2_RHILO	Q984f2 rhizobium l
5	47	56.6	521	2	Q5B5R3_EMENI	Q5b5r3 aspergillus
6	47	56.6	840	1	MCPH1_HYLLA	P61592 hylobates l
7	46	55.4	820	2	Q6DFK4_XENLA	Q6dfk4 xenopus lae
8	46	55.4	1282	2	Q4QJ11_LEIMA	Q4qj11 leishmania
9	46	55.4	1588	2	Q6BUR9_DEBHA	Q6bur9 debaryomyce
10	45	54.2	388	2	Q6RAQ3_BUNHO	Q6raq3 bunopithec
11	45	54.2	407	1	MAGB6_HUMAN	Q8n7x4 homo sapien
12	45	54.2	578	2	Q5V888_HALMA	Q5v888 haloarcula
13	45	54.2	698	2	Q3VBK5_9SPHN	Q3vbk5 sphingopyxi
14	44	53.0	203	2	Q4UBZ7_THEAN	Q4ubz7 theileria a
15	44	53.0	396	2	Q9AGT3_RHIME	Q9agt3 rhizobium m
16	44	53.0	431	2	Q347G4_RHOPA	Q347g4 rhodopseudo
17	44	53.0	431	2	Q6N2D2_RHOPA	Q6n2d2 rhodopseudo
18	44	53.0	450	2	Q3WNV0_9RHIZ	Q3wnv0 mesorhizobi
19	44	53.0	553	2	Q5BAZ3_EMENI	Q5baz3 aspergillus
20	44	53.0	700	2	Q7QQ15_GIALA	Q7qq15 giardia lam
21	44	53.0	1077	2	O97217_LEIMA	O97217 leishmania
22	43	51.8	133	2	Q93JB4_STRCO	Q93jb4 streptomyce
23	43	51.8	138	2	Q3XPX0_9PROT	Q3xpx0 magnetococc

24	43	51.8	147	2	Q5MRI2_DROME	Q5mri2	drosophila
25	43	51.8	232	2	Q9L1M7_STRCO	Q9l1m7	streptomyce
26	43	51.8	255	2	Q415N1_KINRA	Q415n1	kineococcus
27	43	51.8	276	2	Q4DEG9_TRYCR	Q4deg9	trypanosoma
28	43	51.8	284	2	O82397_ARATH	O82397	arabidopsis
29	43	51.8	288	2	Q5MRB0_DROME	Q5mrbo	drosophila
30	43	51.8	288	2	Q5MRB1_DROME	Q5mrbl	drosophila
31	43	51.8	288	2	Q5MRB3_DROME	Q5mrbs	drosophila
32	43	51.8	288	2	Q5MRB5_DROME	Q5mrbs	drosophila
33	43	51.8	288	2	Q5MRB6_DROME	Q5mrbs	drosophila
34	43	51.8	288	2	Q5MRC0_DROME	Q5mrco	drosophila
35	43	51.8	288	2	Q5MRC1_DROME	Q5mrcl	drosophila
36	43	51.8	288	2	Q5MRC8_DROME	Q5mrcl	drosophila
37	43	51.8	288	2	Q5MRC9_DROME	Q5mrcl	drosophila
38	43	51.8	288	2	Q5MRD0_DROME	Q5mrd0	drosophila
39	43	51.8	288	2	Q5MRD1_DROME	Q5mrd1	drosophila
40	43	51.8	288	2	Q5MRD3_DROME	Q5mrd3	drosophila
41	43	51.8	288	2	Q5MRD6_DROME	Q5mrd6	drosophila
42	43	51.8	288	2	Q5MRD8_DROME	Q5mrd8	drosophila
43	43	51.8	288	2	Q5MRE4_DROME	Q5mre4	drosophila
44	43	51.8	288	2	Q5MRH6_DROME	Q5mrh6	drosophila
45	43	51.8	288	2	Q5MRI1_DROME	Q5mri1	drosophila

<!--EndFragment-->

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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:08:23 ; Search time 38.2353 Seconds
(without alignments)
130.855 Million cell updates/sec

Title: US-09-819-144A-2
Perfect score: 268
Sequence: 1 MAAGPRPGAPCRAGAPTIVL.....SSPARATLGKPLVLNDYSLN 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	68	25.4	315	2	C70810	hypothetical prote
2	60.5	22.6	504	2	T33404	hypothetical prote
3	60	22.4	650	2	T48060	beta-D-glucan exoh
4	59	22.0	1687	2	T30176	EGF repeat transme
5	59	22.0	4180	2	G83559	hypothetical prote
6	58.5	21.8	323	2	T19142	hypothetical prote
7	58	21.6	419	2	T36272	hypothetical prote
8	57.5	21.5	886	2	S07132	hypothetical prote
9	57.5	21.5	1611	2	T38236	hypothetical prote
10	57	21.3	308	2	D70875	probable PE protei
11	57	21.3	313	2	A46233	FLAT element-bindi
12	57	21.3	457	2	C70589	probable cobB prot
13	57	21.3	474	2	H86303	hypothetical prote
14	57	21.3	775	2	D86261	hypothetical prote
15	57	21.3	1487	1	EDBEE1	immediate-early pr
16	57	21.3	1487	1	EDBEF6	155K transcription
17	56.5	21.1	136	2	T36547	hypothetical prote
18	56.5	21.1	205	2	C89957	hypothetical prote
19	56.5	21.1	408	2	B87436	conserved hypothet
20	56.5	21.1	640	2	A87715	glucose inhibited
21	56.5	21.1	757	2	T09081	telomere-associate

22	56	20.9	232	2	S24390	transforming prote
23	56	20.9	430	2	T46420	hypothetical prote
24	56	20.9	540	2	S21825	vicilin-like stora
25	56	20.9	616	2	A72627	probable 2-oxoacid
26	56	20.9	780	2	F84470	probable retroelem
27	55.5	20.7	701	2	S61239	hypothetical prote
28	55.5	20.7	1067	2	D75625	probable extracell
29	55.5	20.7	1408	2	S16148	gene serrate prote
30	55.5	20.7	1724	2	T18343	P-glycoprotein - S
31	55	20.5	296	2	A40996	phenylalanine 4-mo
32	55	20.5	323	2	C86384	unknown protein [i
33	55	20.5	352	2	JC2466	inhibin beta-C cha
34	55	20.5	364	1	TVHURL	transforming prote
35	55	20.5	445	2	E87561	hypothetical prote
36	55	20.5	493	2	G84263	long-chain fatty-a
37	55	20.5	513	2	AD1959	ATP-dependent RNA
38	55	20.5	677	2	E70722	hypothetical prote
39	54.5	20.3	251	2	A55523	hypothetical prote
40	54.5	20.3	420	2	AG1859	hypothetical prote
41	54.5	20.3	552	2	E87226	conserved membrane
42	54.5	20.3	848	2	D85635	trimethylamine N-o
43	54.5	20.3	848	2	H90772	trimethylamine N-o
44	54.5	20.3	848	2	C64841	trimethylamine-N-o
45	54	20.1	178	2	T30717	probable virion pr

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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:08:23 ; Search time 11.7647 Seconds
(without alignments)
130.855 Million cell updates/sec

Title: US-09-819-144A-8
Perfect score: 83
Sequence: 1 RRQTLSHGSSSPARAC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	43	51.8	284	2	E84616	probable bHLH tran
2	43	51.8	624	2	T16452	hypothetical prote
3	42	50.6	437	2	S15144	hypothetical prote
4	41.5	50.0	667	2	T46094	hypothetical prote
5	41	49.4	285	2	T29490	hypothetical prote
6	41	49.4	437	2	C35147	integrase homolog
7	41	49.4	470	1	B42746	transcription acti
8	41	49.4	470	1	WZBEA4	transcription acti
9	40	48.2	315	2	C70810	hypothetical prote
10	40	48.2	330	2	G69169	hypothetical prote
11	40	48.2	527	2	S44081	11S globulin - oat
12	40	48.2	593	1	QQBEG6	HWLF1 protein - hu
13	40	48.2	639	2	C95342	nitrous-oxide redu
14	40	48.2	848	2	E71404	hypothetical prote
15	40	48.2	1266	2	I59314	isoleucine-tRNA li
16	40	48.2	1621	2	S62356	TRP-185 protein -
17	39	47.0	108	2	F72469	hypothetical prote
18	39	47.0	168	2	AF3294	peptidoglycan-asso
19	39	47.0	168	2	I40346	omp16 protein - Br
20	39	47.0	177	2	AE3013	omp16 protein [imp
21	39	47.0	177	2	B98271	omp16 protein [imp

22	39	47.0	187	2	S21466	nfxB protein - Pse
23	39	47.0	187	2	B83070	transcription regu
24	39	47.0	209	2	A71800	hypothetical prote
25	39	47.0	248	2	H96831	hypothetical prote
26	39	47.0	513	2	F85095	hypothetical prote
27	39	47.0	571	2	AE3281	hypothetical cytos
28	39	47.0	632	2	H84350	oligopeptidase [im
29	39	47.0	653	2	T01274	hypothetical prote
30	39	47.0	799	2	D85436	MAP3K-like protein
31	39	47.0	960	2	JE0356	gamma-aminobutyric
32	39	47.0	1891	2	T13594	hypothetical prote
33	39	47.0	1920	2	T13893	gene hindsight pro
34	38.5	46.4	158	2	D70755	hypothetical prote
35	38.5	46.4	479	2	T48025	hypothetical prote
36	38	45.8	137	2	T41575	ubiquinol-cytochro
37	38	45.8	203	2	B70784	cytochrome-c oxida
38	38	45.8	245	2	S43293	FLT3/FLK2 ligand (
39	38	45.8	271	2	A96011	probable cell divi
40	38	45.8	355	2	C96651	protein T3P18.9 [i
41	38	45.8	441	2	H70632	hypothetical prote
42	38	45.8	536	2	A45409	atrial natriuretic
43	38	45.8	549	1	F69361	arginyl-tRNA synth
44	38	45.8	735	2	T47594	hypothetical prote
45	38	45.8	960	2	S44812	F44B9.6 protein -

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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:14:58 ; Search time 57.3529 Seconds
(without alignments)
79.361 Million cell updates/sec

Title: US-09-819-144A-2
Perfect score: 268
Sequence: 1 MAAGPRPGAPCRAGAPTIVL.....SSPARATLGKPLVLNDYSLN 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	268	100.0	52	2	US-09-042-225-2	Sequence 2, Appli
2	74	27.6	16	2	US-09-042-225-8	Sequence 8, Appli
3	72.5	27.1	173	2	US-09-252-991A-25321	Sequence 25321, A
4	67.5	25.2	137	2	US-09-252-991A-30540	Sequence 30540, A
5	66	24.6	228	2	US-09-252-991A-28381	Sequence 28381, A
6	65	24.3	166	2	US-09-252-991A-16776	Sequence 16776, A
7	65	24.3	205	2	US-09-252-991A-31167	Sequence 31167, A
8	65	24.3	345	2	US-09-252-991A-25768	Sequence 25768, A
9	64.5	24.1	146	2	US-09-252-991A-25930	Sequence 25930, A
10	64.5	24.1	149	2	US-09-252-991A-30866	Sequence 30866, A
11	63.5	23.7	721	2	US-09-252-991A-28293	Sequence 28293, A
12	63	23.5	128	2	US-10-104-047-3112	Sequence 3112, Ap
13	63	23.5	613	2	US-09-252-991A-19955	Sequence 19955, A
14	63	23.5	1129	2	US-09-252-991A-22330	Sequence 22330, A
15	62	23.1	256	2	US-09-252-991A-25404	Sequence 25404, A
16	62	23.1	328	2	US-09-252-991A-19582	Sequence 19582, A
17	62	23.1	863	2	US-09-252-991A-26099	Sequence 26099, A
18	61.5	22.9	146	2	US-09-949-016-8300	Sequence 8300, Ap

19	61.5	22.9	367	2	US-09-252-991A-19910	Sequence 19910, A
20	61.5	22.9	574	2	US-09-252-991A-30868	Sequence 30868, A
21	61	22.8	170	2	US-09-252-991A-20706	Sequence 20706, A
22	61	22.8	208	2	US-09-252-991A-17849	Sequence 17849, A
23	61	22.8	679	2	US-09-252-991A-27111	Sequence 27111, A
24	60.5	22.6	155	2	US-09-252-991A-32893	Sequence 32893, A
25	60.5	22.6	240	2	US-09-252-991A-28112	Sequence 28112, A
26	60	22.4	343	2	US-09-252-991A-27631	Sequence 27631, A
27	60	22.4	755	2	US-09-902-540-11169	Sequence 11169, A
28	59.5	22.2	158	2	US-09-252-991A-24896	Sequence 24896, A
29	59.5	22.2	293	2	US-09-252-991A-32060	Sequence 32060, A
30	59.5	22.2	395	2	US-09-270-767-44351	Sequence 44351, A
31	59.5	22.2	413	2	US-09-604-231-32	Sequence 32, Appl
32	59.5	22.2	536	2	US-09-359-167-8	Sequence 8, Appli
33	59.5	22.2	606	2	US-09-486-382B-11	Sequence 11, Appl
34	59.5	22.2	683	2	US-09-604-231-30	Sequence 30, Appl
35	59.5	22.2	1031	2	US-09-252-991A-18365	Sequence 18365, A
36	59	22.0	162	2	US-09-252-991A-32101	Sequence 32101, A
37	59	22.0	439	2	US-09-252-991A-17127	Sequence 17127, A
38	59	22.0	770	2	US-09-784-316-5	Sequence 5, Appli
39	59	22.0	770	2	US-10-229-124-5	Sequence 5, Appli
40	58.5	21.8	141	2	US-09-252-991A-23685	Sequence 23685, A
41	58.5	21.8	265	3	US-10-162-335-38	Sequence 38, Appl
42	58.5	21.8	377	2	US-09-252-991A-32966	Sequence 32966, A
43	58.5	21.8	515	2	US-09-252-991A-23632	Sequence 23632, A
44	58.5	21.8	802	2	US-09-252-991A-25050	Sequence 25050, A
45	58.5	21.8	929	2	US-09-252-991A-19203	Sequence 19203, A

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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:14:58 ; Search time 17.6471 Seconds
(without alignments)
79.361 Million cell updates/sec

Title: US-09-819-144A-8
Perfect score: 83
Sequence: 1 RRQTLSHGSSSPARAC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	83	100.0	16	2	US-09-042-225-8	Sequence 8, Appli
2	74	89.2	52	2	US-09-042-225-2	Sequence 2, Appli
3	45	54.2	407	2	US-09-468-433C-26	Sequence 26, Appl
4	44	53.0	336	2	US-09-270-767-34524	Sequence 34524, A
5	44	53.0	336	2	US-09-270-767-49741	Sequence 49741, A
6	43	51.8	199	2	US-09-252-991A-20230	Sequence 20230, A
7	43	51.8	339	2	US-09-270-767-45916	Sequence 45916, A
8	43	51.8	427	2	US-09-252-991A-22649	Sequence 22649, A
9	42	50.6	147	2	US-09-252-991A-26082	Sequence 26082, A
10	42	50.6	215	2	US-09-252-991A-24366	Sequence 24366, A
11	42	50.6	843	2	US-09-252-991A-18927	Sequence 18927, A
12	41.5	50.0	345	2	US-09-252-991A-16990	Sequence 16990, A
13	41	49.4	67	2	US-09-621-976-6000	Sequence 6000, Ap
14	41	49.4	213	2	US-09-252-991A-22647	Sequence 22647, A
15	41	49.4	349	2	US-09-252-991A-30661	Sequence 30661, A
16	41	49.4	470	2	US-10-332-795-3	Sequence 3, Appli
17	41	49.4	831	2	US-09-252-991A-24901	Sequence 24901, A
18	40	48.2	163	2	US-09-252-991A-22928	Sequence 22928, A

19	40	48.2	248	2	US-09-252-991A-22391	Sequence 22391, A
20	40	48.2	562	2	US-09-879-792-12	Sequence 12, Appl
21	40	48.2	1054	2	US-09-949-016-9821	Sequence 9821, Ap
22	40	48.2	1054	2	US-09-949-016-9822	Sequence 9822, Ap
23	40	48.2	1262	2	US-09-357-251-33	Sequence 33, Appl
24	40	48.2	1262	2	US-09-949-016-6182	Sequence 6182, Ap
25	40	48.2	1262	2	US-09-949-016-6850	Sequence 6850, Ap
26	40	48.2	1266	1	US-08-468-557-4	Sequence 4, Appli
27	40	48.2	1266	2	US-09-357-251-32	Sequence 32, Appl
28	40	48.2	1621	1	US-08-242-677-2	Sequence 2, Appli
29	39	47.0	100	2	US-09-390-134B-39	Sequence 39, Appl
30	39	47.0	125	2	US-09-621-976-5826	Sequence 5826, Ap
31	39	47.0	134	2	US-09-252-991A-17233	Sequence 17233, A
32	39	47.0	147	2	US-09-252-991A-28936	Sequence 28936, A
33	39	47.0	178	2	US-09-270-767-32556	Sequence 32556, A
34	39	47.0	178	2	US-09-270-767-47773	Sequence 47773, A
35	39	47.0	186	2	US-09-673-763-12	Sequence 12, Appl
36	39	47.0	212	2	US-09-252-991A-30730	Sequence 30730, A
37	39	47.0	251	2	US-09-252-991A-28124	Sequence 28124, A
38	39	47.0	461	2	US-09-422-936-57	Sequence 57, Appl
39	39	47.0	496	2	US-09-422-936-85	Sequence 85, Appl
40	39	47.0	563	2	US-09-248-796A-17571	Sequence 17571, A
41	39	47.0	578	2	US-09-422-936-55	Sequence 55, Appl
42	39	47.0	581	2	US-09-422-936-59	Sequence 59, Appl
43	39	47.0	581	2	US-09-252-991A-20966	Sequence 20966, A
44	39	47.0	776	2	US-09-252-991A-26717	Sequence 26717, A
45	39	47.0	844	2	US-09-422-936-47	Sequence 47, Appl

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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:31:38 ; Search time 234.765 Seconds
(without alignments)
102.601 Million cell updates/sec

Title: US-09-819-144A-2
Perfect score: 268
Sequence: 1 MAAGPRPGAPCRAGAPTIVL.....SSPARATLGKPLVLNDYSLN 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	268	100.0	52	3	US-09-819-144A-2	Sequence 2, Appli
2	79	29.5	229	4	US-10-425-115-222906	Sequence 222906,
3	77	28.7	190	4	US-10-437-963-198300	Sequence 198300,
4	74	27.6	16	3	US-09-819-144A-8	Sequence 8, Appli
5	73.5	27.4	791	4	US-10-170-385-57	Sequence 57, Appl
6	73.5	27.4	863	4	US-10-359-012-2	Sequence 2, Appli
7	73.5	27.4	863	4	US-10-359-012-14	Sequence 14, Appl
8	73.5	27.4	863	6	US-11-169-041-167	Sequence 167, App
9	71.5	26.7	240	4	US-10-425-115-226148	Sequence 226148,
10	71	26.5	19608	4	US-10-084-846A-8	Sequence 8, Appli
11	70.5	26.3	219	6	US-11-096-568A-18567	Sequence 18567, A
12	70	26.1	497	6	US-11-096-568A-3275	Sequence 3275, Ap
13	70	26.1	498	6	US-11-096-568A-3274	Sequence 3274, Ap
14	70	26.1	498	6	US-11-096-568A-3276	Sequence 3276, Ap
15	70	26.1	550	6	US-11-096-568A-3273	Sequence 3273, Ap
16	68	25.4	315	4	US-10-080-170-423	Sequence 423, App
17	68	25.4	315	4	US-10-080-170-423	Sequence 423, App
18	68	25.4	315	4	US-10-468-356-423	Sequence 423, App
19	67	25.0	219	4	US-10-425-115-262578	Sequence 262578,

20	67	25.0	1321	5	US-10-840-512-117	Sequence 117, App
21	66.5	24.8	185	4	US-10-425-115-341679	Sequence 341679,
22	65.5	24.4	923	5	US-10-756-149-5246	Sequence 5246, Ap
23	64.5	24.1	137	4	US-10-767-701-33507	Sequence 33507, A
24	64.5	24.1	309	5	US-10-450-763-43334	Sequence 43334, A
25	64.5	24.1	596	4	US-10-156-761-8931	Sequence 8931, Ap
26	64	23.9	165	4	US-10-425-115-270067	Sequence 270067,
27	64	23.9	359	4	US-10-437-963-190864	Sequence 190864,
28	63.5	23.7	74	4	US-10-425-115-263976	Sequence 263976,
29	63.5	23.7	87	4	US-10-425-115-313357	Sequence 313357,
30	63.5	23.7	223	4	US-10-425-114-62626	Sequence 62626, A
31	63	23.5	128	4	US-10-104-047-3112	Sequence 3112, Ap
32	63	23.5	128	4	US-10-108-260A-2594	Sequence 2594, Ap
33	63	23.5	128	6	US-11-072-512-3112	Sequence 3112, Ap
34	62.5	23.3	118	4	US-10-424-599-271704	Sequence 271704,
35	62.5	23.3	197	4	US-10-437-963-128246	Sequence 128246,
36	62.5	23.3	208	4	US-10-437-963-176133	Sequence 176133,
37	62.5	23.3	524	5	US-10-450-763-38710	Sequence 38710, A
38	62	23.1	79	4	US-10-425-115-259836	Sequence 259836,
39	62	23.1	175	4	US-10-425-115-210919	Sequence 210919,
40	62	23.1	177	4	US-10-437-963-109208	Sequence 109208,
41	62	23.1	259	4	US-10-443-622-59	Sequence 59, Appl
42	62	23.1	259	5	US-10-974-440-30	Sequence 30, Appl
43	61.5	22.9	135	4	US-10-425-115-350149	Sequence 350149,
44	61.5	22.9	154	4	US-10-767-701-55508	Sequence 55508, A
45	61.5	22.9	170	3	US-09-864-408A-6684	Sequence 6684, Ap

<!--StartFragment-->

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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:31:38 ; Search time 72.2353 Seconds
 (without alignments)
 102.601 Million cell updates/sec

Title: US-09-819-144A-8
 Perfect score: 83
 Sequence: 1 RRQTLSHGSSSPARAC 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : Published_Applications_AA_Main:*
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	100.0	16	3	US-09-819-144A-8	Sequence 8, Appli
2	74	89.2	52	3	US-09-819-144A-2	Sequence 2, Appli
3	51	61.4	415	4	US-10-437-963-145735	Sequence 145735,
4	45	54.2	362	4	US-10-437-963-145733	Sequence 145733,
5	45	54.2	407	4	US-10-085-108-26	Sequence 26, Appl
6	45	54.2	407	4	US-10-108-260A-4444	Sequence 4444, Ap
7	44	53.0	145	5	US-10-773-236-320	Sequence 320, App
8	44	53.0	168	4	US-10-425-115-213570	Sequence 213570,
9	44	53.0	553	6	US-11-188-298-12028	Sequence 12028, A
10	44	53.0	1563	4	US-10-437-963-140084	Sequence 140084,
11	43	51.8	138	4	US-10-437-963-144158	Sequence 144158,
12	43	51.8	198	4	US-10-425-115-199021	Sequence 199021,
13	43	51.8	378	4	US-10-437-963-143718	Sequence 143718,
14	43	51.8	711	4	US-10-437-963-134466	Sequence 134466,
15	43	51.8	735	4	US-10-437-963-120904	Sequence 120904,
16	43	51.8	854	5	US-10-489-425-66	Sequence 66, Appl
17	42	50.6	47	4	US-10-425-115-358602	Sequence 358602,
18	42	50.6	142	6	US-11-096-568A-21109	Sequence 21109, A
19	42	50.6	153	4	US-10-437-963-128233	Sequence 128233,

20	42	50.6	233	4	US-10-425-115-275385	Sequence 275385,
21	42	50.6	566	4	US-10-425-114-47841	Sequence 47841, A
22	41.5	50.0	314	4	US-10-416-090-26	Sequence 26, Appl
23	41	49.4	43	4	US-10-425-115-297323	Sequence 297323,
24	41	49.4	73	4	US-10-767-701-61697	Sequence 61697, A
25	41	49.4	89	4	US-10-437-963-120393	Sequence 120393,
26	41	49.4	89	4	US-10-425-115-357735	Sequence 357735,
27	41	49.4	90	4	US-10-425-115-239337	Sequence 239337,
28	41	49.4	146	4	US-10-437-963-152522	Sequence 152522,
29	41	49.4	157	4	US-10-425-115-359138	Sequence 359138,
30	41	49.4	176	4	US-10-437-963-138329	Sequence 138329,
31	41	49.4	178	4	US-10-264-049-2578	Sequence 2578, Ap
32	41	49.4	189	4	US-10-437-963-149015	Sequence 149015,
33	41	49.4	203	4	US-10-424-599-258595	Sequence 258595,
34	41	49.4	260	4	US-10-437-963-138332	Sequence 138332,
35	41	49.4	412	5	US-10-739-930-10833	Sequence 10833, A
36	41	49.4	470	4	US-10-332-795-3	Sequence 3, Appli
37	41	49.4	470	5	US-10-626-832-8	Sequence 8, Appli
38	41	49.4	740	4	US-10-408-765A-2463	Sequence 2463, Ap
39	41	49.4	835	3	US-09-790-289-3	Sequence 3, Appli
40	41	49.4	835	4	US-10-468-582-3	Sequence 3, Appli
41	41	49.4	835	6	US-11-028-971-3	Sequence 3, Appli
42	41	49.4	1216	5	US-10-450-763-40113	Sequence 40113, A
43	41	49.4	1479	6	US-11-097-143-39600	Sequence 39600, A
44	40.5	48.8	52	4	US-10-029-386-29128	Sequence 29128, A
45	40	48.2	50	4	US-10-425-115-354560	Sequence 354560,

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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:33:48 ; Search time 40.5294 Seconds
(without alignments)
115.804 Million cell updates/sec

Title: US-09-819-144A-2
Perfect score: 268
Sequence: 1 MAAGPRPGAPCRAGAPTIVL.....SSPARATLGKPLVLNDYSLN 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 358988 seqs, 90258633 residues

Total number of hits satisfying chosen parameters: 358988

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	73.5	27.4	791	6	US-10-533-519-66	Sequence 66, Appl
2	73.5	27.4	863	7	US-11-289-102-215	Sequence 215, App
3	73.5	27.4	863	7	US-11-289-102-264	Sequence 264, App
4	70.5	26.3	219	7	US-11-056-355B-8786	Sequence 8786, Ap
5	68	25.4	315	6	US-10-511-244-14	Sequence 14, Appl
6	67	25.0	268	6	US-10-449-902-49268	Sequence 49268, A
7	63	23.5	128	7	US-11-293-697-2594	Sequence 2594, Ap
8	62.5	23.3	208	6	US-10-449-902-34489	Sequence 34489, A
9	62	23.1	259	7	US-11-404-843-59	Sequence 59, Appl
10	61.5	22.9	251	6	US-10-953-349-31645	Sequence 31645, A
11	61.5	22.9	251	7	US-11-056-355B-68137	Sequence 68137, A
12	61.5	22.9	406	6	US-10-953-349-31643	Sequence 31643, A
13	61.5	22.9	406	7	US-11-056-355B-68135	Sequence 68135, A
14	61	22.8	200	6	US-10-449-902-38799	Sequence 38799, A
15	61	22.8	656	7	US-11-293-697-2611	Sequence 2611, Ap
16	60	22.4	67	6	US-10-510-953-114	Sequence 114, App
17	60	22.4	668	6	US-10-449-902-41400	Sequence 41400, A

18	59.5	22.2	233	6	US-10-449-902-50882	Sequence 50882, A
19	59.5	22.2	525	6	US-10-449-902-28853	Sequence 28853, A
20	59.5	22.2	606	6	US-10-449-902-36757	Sequence 36757, A
21	59.5	22.2	683	6	US-10-805-394-6961	Sequence 6961, Ap
22	58.5	21.8	212	6	US-10-449-902-30492	Sequence 30492, A
23	58.5	21.8	375	7	US-11-056-355B-3621	Sequence 3621, Ap
24	58	21.6	139	7	US-11-293-697-4026	Sequence 4026, Ap
25	58	21.6	240	6	US-10-953-349-34415	Sequence 34415, A
26	58	21.6	330	6	US-10-449-902-29084	Sequence 29084, A
27	58	21.6	330	6	US-10-449-902-31752	Sequence 31752, A
28	58	21.6	330	6	US-10-449-902-51679	Sequence 51679, A
29	58	21.6	442	7	US-11-330-403-7420	Sequence 7420, Ap
30	57.5	21.5	108	7	US-11-056-355B-11267	Sequence 11267, A
31	57.5	21.5	500	6	US-10-533-232A-12	Sequence 12, Appl
32	57.5	21.5	784	6	US-10-449-902-41427	Sequence 41427, A
33	57.5	21.5	1308	7	US-11-358-419-79	Sequence 79, Appl
34	57.5	21.5	3934	7	US-11-165-586-20	Sequence 20, Appl
35	57	21.3	170	6	US-10-953-349-34677	Sequence 34677, A
36	57	21.3	226	6	US-10-553-436-253	Sequence 253, App
37	57	21.3	255	7	US-11-056-355B-63435	Sequence 63435, A
38	57	21.3	260	7	US-11-366-001-65	Sequence 65, Appl
39	57	21.3	291	6	US-10-553-436-251	Sequence 251, App
40	57	21.3	295	7	US-11-056-355B-63434	Sequence 63434, A
41	57	21.3	311	6	US-10-540-898-364	Sequence 364, App
42	57	21.3	575	6	US-10-131-833A-128	Sequence 128, App
43	56.5	21.1	125	6	US-10-953-349-35765	Sequence 35765, A
44	56.5	21.1	125	7	US-11-056-355B-2376	Sequence 2376, Ap
45	56.5	21.1	125	7	US-11-056-355B-7679	Sequence 7679, Ap

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OM protein - protein search, using sw model

Run on: December 9, 2006, 04:33:48 ; Search time 12.4706 Seconds
(without alignments)
115.804 Million cell updates/sec

Title: US-09-819-144A-8
Perfect score: 83
Sequence: 1 RRQTLSHGSSSPARAC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 358988 seqs, 90258633 residues

Total number of hits satisfying chosen parameters: 358988

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	45	54.2	407	7	US-11-293-697-4444	Sequence 4444, Ap
2	44	53.0	554	6	US-10-449-902-45925	Sequence 45925, A
3	43	51.8	231	7	US-11-056-355B-77142	Sequence 77142, A
4	43	51.8	247	7	US-11-056-355B-77141	Sequence 77141, A
5	43	51.8	295	7	US-11-056-355B-77140	Sequence 77140, A
6	43	51.8	399	6	US-10-449-902-49082	Sequence 49082, A
7	42	50.6	142	7	US-11-056-355B-6136	Sequence 6136, Ap
8	41	49.4	123	6	US-10-953-349-28944	Sequence 28944, A
9	41	49.4	813	7	US-11-056-355B-44911	Sequence 44911, A
10	40	48.2	183	6	US-10-953-349-7832	Sequence 7832, Ap
11	40	48.2	183	7	US-11-056-355B-43969	Sequence 43969, A
12	40	48.2	212	6	US-10-953-349-7831	Sequence 7831, Ap
13	40	48.2	212	7	US-11-056-355B-43968	Sequence 43968, A
14	40	48.2	212	7	US-11-056-355B-105128	Sequence 105128,
15	40	48.2	212	7	US-11-056-355B-116367	Sequence 116367,
16	40	48.2	234	6	US-10-953-349-7830	Sequence 7830, Ap
17	40	48.2	234	7	US-11-056-355B-43967	Sequence 43967, A

18.	40	48.2	234	7	US-11-056-355B-105127	Sequence 105127,
19	40	48.2	234	7	US-11-056-355B-116366	Sequence 116366,
20	40	48.2	245	7	US-11-056-355B-105126	Sequence 105126,
21	40	48.2	245	7	US-11-056-355B-116365	Sequence 116365,
22	40	48.2	315	6	US-10-511-244-14	Sequence 14, Appl
23	40	48.2	462	6	US-10-540-898-581	Sequence 581, App
24	40	48.2	623	6	US-10-449-902-45260	Sequence 45260, A
25	40	48.2	623	6	US-10-449-902-45686	Sequence 45686, A
26	40	48.2	1262	6	US-10-533-519-934	Sequence 934, App
27	39	47.0	86	7	US-11-056-355B-60672	Sequence 60672, A
28	39	47.0	97	7	US-11-056-355B-60671	Sequence 60671, A
29	39	47.0	120	6	US-10-510-953-183	Sequence 183, App
30	39	47.0	144	7	US-11-056-355B-63175	Sequence 63175, A
31	39	47.0	167	7	US-11-056-355B-63174	Sequence 63174, A
32	39	47.0	175	7	US-11-056-355B-23148	Sequence 23148, A
33	39	47.0	175	7	US-11-056-355B-105914	Sequence 105914,
34	39	47.0	175	7	US-11-056-355B-117153	Sequence 117153,
35	39	47.0	195	7	US-11-056-355B-63173	Sequence 63173, A
36	39	47.0	237	6	US-10-953-349-28670	Sequence 28670, A
37	39	47.0	248	7	US-11-056-355B-23147	Sequence 23147, A
38	39	47.0	248	7	US-11-056-355B-105913	Sequence 105913,
39	39	47.0	248	7	US-11-056-355B-117152	Sequence 117152,
40	39	47.0	336	7	US-11-056-355B-84015	Sequence 84015, A
41	39	47.0	362	7	US-11-174-307B-4204	Sequence 4204, Ap
42	39	47.0	450	6	US-10-449-902-37895	Sequence 37895, A
43	39	47.0	476	6	US-10-449-902-47026	Sequence 47026, A
44	39	47.0	790	6	US-10-449-902-41114	Sequence 41114, A
45	39	47.0	960	7	US-11-384-109-2	Sequence 2, Appli